

Fig. 1

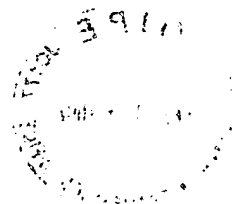
HP02573 61' YGRQDLHLRIFDPSPIEDARADNIFTATERNRIDYVSSAVRIDHAPDLPRPEVCFIGRSN
Cgpa 1"* * * * *
MFFAQPVSFIMGAVRMDAMPSPDLPEVAFAGRSN

HP02573 121' VGKSSLIKALFSLAPEVEVRVSKKPGHTKKMNEFFKVGHFTVVDMPGYCF----RAPED
Cgpa ***** * * * * *
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HP02573 176' FVDMVETYLKERRNLKRTFLLVDSVVVGIQKTDNIAIEMCEEALPYVIVLTKIDKSSKGH
Cgpa * * * * *
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HP02573 236' LLKQVLQIQKFVNMKTQGCFFPQLFPVSAVTFSGIHLRCFIASVTGSLD
Cgpa * * * * *
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HP02573 153" VDKVVAETQKAIKRAAA-FPRVLATSSSEKGLGMPRELRAEIVRLCIDE



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HP02612   61'   KVPLAGGGRKPRLLHRRHRVYKLVEDTKHRPKENLELILTQSVENVGVRGDLVSVKKSLGR  
          ..****... * ** *..*** **  
RL9_MYCLE 1"      MKLILTADV D H L G S V G D T F E V K D G Y G R  
  
HP02612   121'  NRLLPQGLAVYASPENKKLFEEKKLLRQEGKLEKIQTKA GEALGVVVAPHTILKLP AEPIT  
          * ***.****. ****. . * *. * . ....*. * .. * *** .....  
RL9_MYCLE 28"  NFLLPHGLAIVASRGAQRQA DEIRRAR -ETKAMRDREHANEIKVAIEALGSVSLPMKTVA  
  
HP02612   181'  RWGEYWCEVTVNGLDTVRVPM SVVNFEKPKTKRYKYWL AQQA AKAMAPTSPQI  
          * . . **.****. . . * . * . . .  
RL9_MYCLE 87"  DSGKLFGSVTAGDVVA I KKAGGNLDKRIVLR PKTHIKAVGTHPVSVHLHPEVDVVVLL
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HP02612 61' KVPLAGGGRKPRLHRRHRVYKLVEDTKHRPKENLELILTQSVENVGVRGDLVSVKKSIGR

[illegible]

MKLLILTADV D H L G S V G D T V E V K D G Y G R

HP02612 121' NRLLPQGLAVYASPENKKLFEEKKLLRQEGKLEKIQTKAGEALGVVAPHTLKLPAEPIIT

[illegible]

RL9_MYCLE 28" NFLPHGLAIVASRGAQRQADEIRRAR-ETKAMRDREHANEIKVAIEALGSVSLPMKTIVA

RWGEYWCETVTVNGLDTVRVPM SVVNF EKP KTKRYKYWLAQQAAKAMAPTSPQI

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RL9_MYCLE 87" DSGKLFSGSVTAGDVVAAIKKAGGNLDKRIVRLPKTHIKAVGTHPVSVHLHPEVDVVLL

Fig. 3

HP10117	61'	KAKGKGQSQTRVNINAALVEDIINLEEVNEEMKSVIEALKDNFNKTNIRTSFGSLDKIA
RRF_BRUME	1"	..* * **** * . * . * . * . * . MSDAFDINDLKRRMEGAVNALKHDLGGLRTGRASASLLEPIT
HP10117	121'	VVTADGKLALNQISQISMKSPQLILVNMAFPECTAAAI-KAIRESGMNLNPEVEGTLIR
RRF_BRUME	43" ** . * * * * . * IEAYGSTMPINQVANISV--PESRMLSVSVWDKSMVGAVERAIRDSGLGLNPITDGMTLR
HP10117	180'	VPIPVQVTRHREMLVKLAKQNTNKAQKSLRKVRNMSMNKLLK-SKDT-VSEDTIRLIEKQ
RRF_BRUME	101"	...* * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . IRLPELNEQRRKELVKIAHQYAEQGRARIAARHVRRDGMQDLKKLEKDSVISQDESRVLSEK
HP10117	238'	ISQMADDTVAELDRHLAVKTKELLG
RRF_BRUME	161" * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . VQKLTDGDTIAEMDKIVAVKEGEIMQV

Fig. 4

HP10120 1' MQRVSGLLSWTLSTLWLSGLSEPGAARQPRIMEE-KALEVYDLIRTIRDPEKPNLTLEEL
 CEF45G2 1" MGQERLDNANPTLEFDSKPRHRPVTGTERDESVEPDFDSWEIFDLIRDINDPEHPYTYLEQL
 HP10120 60' EVVSESCVEVQINEEYLVIIIRFTPTVPHCSLATLIVGNLHF
 CEF45G2 61" NVVQEELIKV-FIDEETFVKVNFPTTIPHCSMATLIGLAIRVKLLRSLRHPKVKVSVSIT

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Fig. 5

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HP10582	1'	MDSNHQSNYKLSKTEKKFLRKQIKAKHTLLRHE-GIETVSYATQSLVVANGGLGN
YKY5_CAEEL	361"	RELSYFNTEKAKRIGERFEGGKLAQKVHKSIEQLKRHPDVQISTEPTKYLLVSNSSILC
HP10582	55'	GVSRNQLLPV-LEKCGLVDALIMPKNKPYSFARYRTTEESKRAYVTINGKEVVDDLQKQI
YKY5_CAEEL	421"	GVSLLEELEEIFLPLDELAEFIVYPNKRYSFVQCSSIEKSIQVTELHGLIPPSLKNSHQ
HP10582	114'	TYLNLNFEKVQWKELRPQALPPGLMVVEEIIISSEEKMLLESVDWTEDTDNQNSQKSLKH
YKY5_CAEEL	481"	PFAISYVENLPEATKCEDFRPANLKIIEEYVSSDLEKELVDLV-----TNHPSVQSLKH
HP10582	174'	RRVKHFGYEFHYENNNVDKDKPLSGGLPDICESFLEKWLKGYIKHKPDQMTINQYEPGQ
YKY5_CAEEL	535"	RAVVHFGHVFDYSTNSASEWKE-ADPIPPVINSLIDRLISDKYITERPDQVTANVYESGH
HP10582	234'	GIPAHIDTHSAFEDEIVSLSLGSEIVMDFKH--PDGIAVPVMLPRRSLLVMTGESRYLWT
YKY5_CAEEL	594"	GIPSHYDTHSAFDDPIVSISSLSDVVMFEKDGANSARIAPVLLKARSLCLIQGESRYRWK
HP10582	292'	HGITCRKFFDTVQASESLKSGIITSDVGDLTLSKRGLRTSFTFRKVRQTPCNCISYPLVCD
YKY5_CAEEL	654"	HGIVNRKYD-----V-----DPRTRVVPROTNRVSLTLRKIRKPCCEWKEFCDW

...the ...

Fig. 6-1

HP10582	352'	Q R K E T P S F P E S D K E A S R L E Q E Y V H Q V Y E E I A G H F S S T R H T P W P H I V E F L K A L P S G S I V A .* ** * . *
YKY5_CAEEL	700"	D R K G E - M S V P S N E D L A L K L E N S Y S D V Y E N I A S H F D E T R H S S W K A V K Q F I N E I P R G S V M Y
HP10582	412'	D I G C G N G K Y L G I N K E L Y M E R R V A A L Q E I V R L L R P G G K A L I Y V W A M E Q E Y N K Q K S K Y L R G N *. ***** * * * * * * *
YKY5_CAEEL	759"	D V G C G N G K Y L - I P K D G L L K I G C D M C M G L C D I A R K K D C H V A R C D A L A L P F ----- R Y E S A D
HP10582	472'	R N S Q G K K E E M N S D T S V Q R S L V E Q M R D M G S R D S A S S V P R I N D S Q E G G C N S R Q V S N S K L P V H * * * * * *
YKY5_CAEEL	813"	A A I S I A V L H H I A T F E R R K R L I E E L L R V V K P G S K I C V T - V W S M D Q S Q S E Y A K M R G N K D D V -
HP10582	532'	V N R T S F Y S Q D V L V P W H L K G N P D K G - K P V E F G P I G S Q D P S P V F H R Y Y H V F R E G E L E G A C R * * * * * * * * *
YKY5_CAEEL	871"	A A A P A V S S E E T Q T T N R L K V H D G K D F E Q Q D V L V P W T I D Q K G E T F L R Y Y H V F R E G E A E K L I E
HP10582	591'	T V S D V R I L Q S Y D Q G N W C V I L Q K A * * * *
YKY5_CAEEL	931"	S V Q G C K L I S V E K E Q G N Y - I I I A K K I

Fig. 7

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HP10149	1'	MAMSFEPWQYRFPFFFTLQPNVDTRQQLAAWCSLVLSFCRLHKQSSMTVMEA *.*****
W02A11	1"	MAAATTTASAFKWPWQYDFPFFTIQKSLNTKDKQLEAWARLVIDYAQHKNKIYSLDIAEA *.*****
HP10149	55'	QESPLFNNVKLQKLPVESIQIVLEELRKKGNLEWLDKSKSSFLLIMWRRRPEEWGKLIYQW *.*****
W02A11	61"	TTSELFNNQKLNRRRLSTDGVNTVLQYLEQKKLIEFTDNGRTRFRHFWRRRPDVWANMIYQW *.*****
HP10149	115'	VSRSGQNNSVFTLYELTNGEDTEDEEFHGLDEATLLRALQALQOEHKAEIITV-SDGRGV *.*****
W02A11	121"	AVENAFINTPLTYEITHGDDTTNESFHNLEREILMKALTCLEEQRRRAQLMNIIGDNEGV *.*****
HP10149	174'	KFF **.
W02A11	181"	KFI

Fig. 8

HP10160 1' MASRGKTETSKLKQNLQEQDLRLMQQLQDLQECREELDTDEYEETKKTLEQLSEFNDSL
 ZK1248 1" MGVDLLIKNAQKTIDRLIRQLAEIEQEENNLEDEYRELREDTVNLQEQYQKIV
 HP10160 61' KKIMSGNMTLVDELQSGMQLAIQAAISQAFKTPVIRLFAKKQPGQLRTRLAEMDRDLNVG
 (ZK1248 56" ERLQGGDVSLIDDLTATKIAIRMAISKAFTKTPHMAITAGZHTGLLREKLMNTETNYSQ
 HP10160 121' KLERDLYTQQKVEILTALRKIGELKTADDEAFLSANAGAILSQFEKVTDLGSGDKIILAL
 ZK1248 116" KMPKQGYLERKFEILMALRRLEETLTEDERKFLSDRLET--PEFQLIEANANRLFSGNVT
 HP10160 181' ASFEVEKTKK
 ZK1248 174" SPVFRVQIMASPKPKKVRLLDDKTENVSPWKAWHTTEKKRKFYTNDKTKESLWDHPNTR

HP10173

1' MKLLTHNLSSHVGVGSRGFPLRLQATEVRICPVEFNPFVARMIPKVEWSAFLEAADN
***...**. . ***. * ..*. *.*.. *

C04H5

1" MKLFFVNFMSSRFLKNVTVGYPINLVVKQFVEKDIEFRDNTIVMLDRIQEALIVAAAA

HP10173 61' LRLIQ-VPKGPVEGYEE-NEEFLRTMHHLLLEVEVIEGTLQCPESGRMFPISRGIPNMLL
 . . . * . . * . . * . . * . . * . . * . . * . . * . . * . . * . . *

C04H5 61" VNQSDRIPREKPEKWDELTDDEQLRVFHHLMNDIVIDGELICPETKTVPFPIDRGIPNMULK

HP10173 119' SEETES
C04H5 121" VDAEK
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CELL#55F8 263"

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CELL#55F8 323" -----ALIVAPTRRELVIQIMKHINALISTITQLIAT

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CELL#55F8 383" SI VGG LA QV KQ ER I I S Q O R P D I V V A T P G R L W A M M O E A E T G E F L A E W K D I L K C L V D E T D R M

[illegible]

CELL#55F8 443" VEEGYFAELTHILNKIHEESEKELOTLVFSATLTFAKAODVAEEKKKAKELSSOOKIQ

[illegible]

CELL#55F8 503" RL IKLTGLRENKHKVIDLTRQMGTA GCLVEAR INCGNLLLEKDTSLVYLLTRYPGRTIVFV

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Fig. 10-2

HP02644 595' NSISCIKRLSGLLKVLDDIMPLTLHACMHQKQRLRNLEQFARLEDCVLLATDVAARGLDIP
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CELLF55F8 563" NSIDAARRLYSVLKSVNIDPMILHAKMIQKQRLKNLEKFSSEKNAVLLATDVAARGLDIQ
HP02644 655' KVQHVHYQVPRTSEIYVHRSGRATARATNEGLSLMLIGPEDVINFKKIYKTLKDEDIPL
.. ***** .. ***. ***** .. **...*...* .. **...*...*...
CELLF55F8 623" GIDHVIHYQVPKKVEIYIHRSGRTARASHERGLTVVLVDPSPSRQFYMKLCCKGLNFMQDLNV
HP02644 715' FFPVQ-TKYMVVKERIRLARQIEKSEYRNFOACLNSWIEQAAALEIELEEDMKKGKA
***. . *...*. *...*. *...*. *...* . . . *...*. *...* . . . *...*. *...* . .
CELLF55F8 683" FPIDFEPLMNAIKKRVRLASEIDSLGFRCKKIDMSESWFEKAAARAADLDYDETRHREMDG
HP02644 774' DQOEERRRQKQMKVLKKELRHLLSQPLFTESQTKKYPTQSGKPFLLVSAPSKSESALSCL
* * * * * * * * *
CELLF55F8 743" LNLEVDTMVQKSRLQQAQLRTELSLPLPRVDGSDSMKTKYITPEIVARLSVGDNAIDVL
HP02644 834' S-KQKKKKTKKPKPEQPEQPPSTSAN
* *
CELLF55F8 803" NQKIDETKEWKRKSRKATREDEMNMKKSLKSSQKNQERLAEKKQCKAAKVTKLSETD

Fig. 11

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HP03233 1' MAAPGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQEKRAAEETHFGFETVS
      ...*.* * * * * * .. . .... *****..
SPUBM 1" MSRLRAPVAKFLADGLKGI RSTALAGSRLSN-CRYTSTS KOTDTSSHMTHTFGFKDVP

HP03233 61' EEEKGGKVYQVFESVAKKYDVMMNDMSLG IHRVWKOLLWKMHPLPGT---QLLDVAGGT
      *.*. * **.....*** *****.**....**..* ..*****
SPUBM 58" EDEKEHLVKNVFTSSVAKKYDEMNDAMSLGIHRLWKNIFVSR LNPNGNSTVPMKILDVAGGT

HP03233 118' GDIAFRFLN VQSQHQRKKRQLRAQQNL SWEELAKEYN EEDSLGGRVVVC DINKEML
      *****... ..*..*
SPUBM 118" GDIAFRILNHATNHNGDRNTRVIV-----ADINPDM L

HP03233 178' KVG-KQKALA QGYRAG-LAWVLGDAEEL-PFDDDKFDIYTFIAGIRNVTHIDQALQE AHR
      **. . . . * * * * . *...* .....* * * * ..*..*
SPUBM 150" SVGLRRSKKTPPYDSGRVEFFIEQNAE ILDKIPDNSIDMYTTFIAGIRNCTHIPKVLEQA YR

HP03233 235' VLKPGGRFLCLEFSQVNPNPLISRLYDYLSFQVIPVLGEVIAGDWKS YQYLVESIRRFPSQ
      ***** * ****** . . . ** .....*...* .....* .....*
SPUBM 210" VLKPGGVFSCLEFSKVYPAPLAELYRQYSFKILPLL GTTIAGDSQSYEYLVESIERFP DA

HP03233 295' EEFKDMIEDAGF---HKVTYESLTSGIVAIHSGFKL
      .. .***** .....*..* .....*..*
SPUBM 270" KTFAKMIEDAGFTLAGETGYETLSFGIAAHTGIKL

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[illegible]

HP10437 1' MQKSCENEKGKPNMPKAEEDRPLEDPQAEAGNPQPSSEGVSQAEAGNPRGGPNQPGQG

[illegible]

1" MKSCQKMEGKPN-----ESEPKEHEEPKPEEKPEEEKLEEEAKAKGTFRERLIQSLQOE
pp21

HP10437 61' FKEDTPVRHLDPEEMIRGVDELERLREEIRRVNRKFMHWHKQHSRSPYPVCFRP

[illegible]

pp21 56" FKEDIHNRHLSNEDMFREVDEI-----DEIRRVNRKLIIVMRKKNRNRNHPYPYILM

Fig. 13

HP10525 1' MELSAYLREKLQDLEAEHVEVEDTTLNRCSCSFRVLVVSAKFEKPLLQHRHRLVNA
 SPAC8C9 1" MVNAQQLELLIQTLEPTHEIQDM-SGGCGQNFVEIIVSPLEFEGKSTLARHRLVNHKL
 HP10525 61' AEELPHIHAFEQ-KTLTPDQWARERQK
 SPAC8C9 59" QEVIKDIHAFTQVRTLSFRHIR

Fig. 15

HP03090 1' MAARRALHFVFKVGNRFQTARFYRDVLGMKVLRHEEFEEGCKAACNGPYDGKWSKTMVGF
 CEHYPO 1" MTARALHYVFKVANRAKTIDFFTNVLNMKVLRHEEFEEGCEATCNGPYNGRWSKTMIGY
 HP03090 61' GPEDDHFVAELTYNYGVGDYKLGNDFMGITLASSQAVSNARKLEWPLTEVAEGVFETEAP
 CEHYPO 60" GSEDEHFVLEITYNYPIHKYELGNDYRAIVIDSDQLFEKVEKIN--HRKSGCGRLAVKDP
 HP03090 121' GGYKFYLNRSRSLPQSDPVLKVTLAVSDLQKSLNYWCNLLGMKIYEKDEEKQRALLGYADN
 CEHYPO 118" DGHEF--KIGKADQSPKVLRVQNVNVDLEKSKKYWNETLGMPIVEEKSRRIR--MSYGDG
 HP03090 181' QCKLELQGVKGGVDHAAAFGRIAFSCPQKELPDIEDLMKRENQKILTPLVSLDTPGKATV
 CEHYPO 174" QCELEIVKSQDKIDRKTGFGRIAFSYPEDKLESLQDKIKSANGTIINELTLETPGKADV
 HP03090 241' QVVILADPDGHEICFVGDEAFRELSKMDPEGSKLLDDAMAADKSDWEFAKHNKPKASG
 CEHYPO 234" QVVILADPDGHEICFVGDEGFRALSKIDDKAESSELKEQIKKDDSEKWI

Fig. 16

HP03145	1'	MLGSRAAGFARGLRALALAWLPWGRGRSFALARAAAGPHGGDLQPPACPEPRGRQLSLSA
SCCOQ2	1"	MIIKPIASPARYFLRTPSWSAVAIFQAVKIKPLQLRTNSSNSVTPNLISPSK
HP03145	61'	AAVDSAPRPLQPYLRIMRLDKPIGTWLLYLPCTWSIGLAA---EPGCCFPDWYMLSLFGT
SCCOQ2	53"	KSWKDLFSKRWQYYAEISRAGSPTGTYYLLYSPCTWSILMAAYAYDSSLVNVTKMLALFGV
HP03145	118'	GAILMRGAGCTINDMWDQDYDKKVTRTANRPIAAGDISTFQSFVFLGGQLTALGVLLCL
SCCOQ2	113"	GSFLMRGAGCVINDLWDRELDKAKVERSKSRPLASGKLSVRQAISSLVQLTASLGILLQL
HP03145	178'	NYYSIALGAGSLLLVITYPLMKRISYWPQLALGLTFNWGALLGWSAIGK-SC-DPSVCLP
SCCOQ2	173"	NPYTIKLGVASLVPVCIYPAMKRITYYPQVVVLGLTFGYGAVMGWPALAGEACMNWSVVAP
HP03145	236'	LYFSGVMWTLIYDTIYAHQDKRDDVLIGLKS TALRFGENTKPLSGFSVAMLGALSLVG
SCCOQ2	233"	LYLSTISWIVLYDTIYAHQDKRDDVKANIYSTALRFGDNTKPVLCGLAALQIATLATAGI
HP03145	296'	NSGQTAPYYA-ALGAVGAHLTHQIYTLDIHRPEDCWNKFISNRTLGLIVFLGIVLGNLWK
SCCOQ2	293"	MNGQGPVFFYTLGVAGAYRLSSMIYKVDLDDPKDCFRWFKRNSNTGYLVAAAIALDWLAK
HP03145	355'	EKKTDKTKKGIENKIEN
SCCOQ2	353"	SFIYDS

Fig. 17

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HP03185 1' MSGRSGKKKMSKLRSARAGVIFPVGRMLRYLKKGTFKYRISVGAPVYMAAVIEYLAAE
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MH2A1.2 1" MSSRGKKSTKTSRSKAGVIFPVRMLRYIKKGHPKYRIGVGAPVYMAAVLEYLTAEI

HP03185 61' LELAGNAARDNKKARIAPRHILLAVANDEELNQLLKGVTIASGGVLPRIHPELLAKKRGT
*****.*..***** ***** ***** ***** ***** *****
MH2A1.2 61" LELAGNAARDNKKGRVTPRHILLAVANDEELNQLLKGVTIASGGVLPNIHPELLAKKRGS

HP03185 121' KGKSETILSPPEKRRKATSGKGGKSKAAKPRTSKSKPKDSKEGTSNSTSEDGPG
*** *.* **.* * ..*. * ..*. * ..*. * ..*. * ..*. * ..*. * ..*.
MH2A1.2 121" KGKLEAIITPPPAKKAKSPSQKKPVSKKAGGKKGARKSKKKQGEVSKAASADSTTEGTPA

HP03185 181' DGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHPTTAEIDLKEDIGKALEKAGGKE
****.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*
MH2A1.2 181" DGFTVLSTKSFLGQKLNLIHSEISNLAGEFEVAIINPTNADIDPKDDDLGNTLEKKGKKE

HP03185 241' FLETVKELRKSGPLEVAEAAVSQSGLAAKFVIHCIPQWGS DKCEEQLEETIKNCLSA
*.*.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*
MH2A1.2 241" FVEAVLELRKKNGPLEVAGAAVSAGHGLPAKFVIHCNSPVWGADKCEELLEKTVMKNCLAL

HP03185 301' AEDKKLKSVAFPFPPS GRNCFPQTAAQVTILKAISAHFDDSSASSLKNVYFLFDSESIG
*.*.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*
MH2A1.2 301" ADDKKLKSIAFPSIGSRNGFPQTAAQILKAISSYFVSTMSSSIKTVYFVLFDESIG

HP03185 361' IYVQEMAKLDAK
*****
MH2A1.2 361" IYVQEMAKLDAN

```

Fig. 18

18/35

HP03324	1'	MALCALTRALRSNLAPPTVAAPAPSLFPAAQMMNGLLQQPSALMLLPCRPVLTVALN
BRPL2	1"	MGLKRFPVTPGRRFMVI
HP03324	61'	ANFVSWKSRTKYTITPVKMRKSGGRDHTGRIRVHGIGGGHKQRYRMIDFLRFRPEETKSG ..***.* **.* **.* **.* **.* **.* **.* **.*
BRPL2	19"	SDFS DITKTEPEKSLLAPLKTGGRNHHGRVTVRHRGGGHHKRRYRIIDFKRY----DKAG
HP03324	121'	PFEKVIQVRYDPCRSADIALVA-GGSRKRWIIATENMQAGDTILNSNHIGRMAVAAREG .***... *** *** ***. ... **.* **.* **.* **.* **.* **.*
BRPL2	75"	-IPAKVLAIEYDPNRSARIAALLLYADGEKRYIILAPKGVNVGDTLMSGPD---AEIRP--G
HP03324	180'	DAHPLGALPVGTLINNVESEPGRGAQYIRAAGAGNVRNSRPSIQR .* **.* **.* **.* **.* **.* **.* **.*
BRPL2	129"	NALPLEKIPVGTLVHNVEFTPGKGGQIARAAGTYCQIMAKEGNVALLRMPSPGELRKVHIK

Fig. 19

19/35

HP10648 181' LTPRPGSPRGQHEPSKPPPAGEVTGTGGFAGAKKRGSSSQAPASKKLNKEELPVIKGP

CEY40B1B 1" MSTGANLLVMNDTC

HP10648 241' KSGRVWKDRSKKRFSQMLQDKPLRTSWQRKMKERQERKLAKDFARHLEEEKERRRQEKQ

CEY40B1B 15" KSNRWKTKQEKKHSEIKKVTKLSTWDKMKELKAKDMVKRVQDNIREKQVQERQEKKE

HP10648 301' RRAENLKRRLENERKAEVVQVIRNPAKLKRAKKQLRSIEKRDTLALLQKQPPQPAKI

CEY40B1B 75" RKVEQEKRRLENERKAEIVQKITKIHKLKKTKKRQLRSIQMRDTTQVTK

Fig. 20

HP10162	1'	MEPQERETQVAAWLKKIFGDHPI PQYEVNPRTEILHLSENRVRDRDVYLVIEDLKQ *..**...***.*****.*****.*.*****.*****.*****.*****.
RNUNK	1"	MAALEEKASQVAEWLKKIFGDHPI PQYEMNARTTEILYHLSENRVRDRDVNLVIEDLRP
HP10162	61'	KASEYESEAKYLQDLIMESVNFPANLSSTGSRYNALVDSAVALETKDTSLASFIPAVN ***** **..*****.*****.*****.*****.*****.*****.*****.
RNUNK	61"	KASEYESEAKRLEDFLMESVNFPANLSNTGSRFLNALVDSAIALEIKDTSIASFIPAVN
HP10162	121'	DLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDVKKAELHLSTERAKVDNRRQ *****.*****.**.*****.*****.*****.*****.*****.*****.
RNUNK	121"	DLTSDLFRTKSKSEEIKLELGKLEKNLTATLVLEKCLREDLKKADVHLSAERAKAEGRQL
HP10162	181'	NMDFLKAKSEEFRTGFKAAEEQLSARGMDASLSHQSLVALSEKLARLKQQTPLKKKKLES *****..*****.*****.*****.*****.*****.*****.*****.
RNUNK	181"	NMDFLKAKAAEFRFGIRAAEEQLSSRGMDASLSHRSLVALSDKLSELKQQTPLKKKKLES
HP10162	241'	YLDLMPNPFSLAQVKIEEAKRELDSEIELTRRRVDMMEL *****.*****.*****.*****.*****.*****.*****.
RNUNK	241"	YLDLMPNPFSLAQVKIEEAKRELDIAEALTCKKVDMMEL

KAT--PPQIVNGDQYCGDYELFVEAVEQNTLQEEFLKLA
 *** *..*** * * * * * * * * * * * * * * * *
 ..

22/35

22/35

Fig. 23

HP10559	1'	MPVKKRKRSPGVAAVAEDGGLKKCKISSYCRSQPPARLISGE
KIAA	61"	QTGSLRSCSSDCFNKVMPPRRKRR-----PASGDDLSAKKSRHDSMYRKYDSTRIKTEE
HP10559	44'	EHFSSKKCLAWFYEYAGPDEVVGPEGMKFCEDIGVEPENIIMLVLAWKLEAESMGFFTK
KIAA	116"	EAFFSKRCLEWIFYEYAGTDDVVGPEGMKFCEDIGVEPENVMVLVLAWKLDAQNMGYFTL
HP10559	104'	EEWLKGMTISLQCDCTEKLQNKDFELRSQNDISSFKNIYRYAFDFARDKQDQSLDIDTAK
KIAA	176"	QEWLKGMTISLQCDTTEKLIRNTLDYLRSLNDSTNFKLLIYRYAFDFAREKDQDQSLDINTAK
HP10559	164'	SMLALLIGRTWPLFSVFFYQYLEQSKYRVMNKDQWYNVLEFSRTVHADLSNYDEDEDGAWPVL
KIAA	236"	CMGLLLLGKIWPLFPVFHQFLEQSKYKVINCKDQWCNVLEFSRTINLDLSNYDEDEDGAWPVL
HP10559	224'	LDEFVEWQKVRQTS
KIAA	296"	LDEFVEWYKDKQMS

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HP10562 61' QESEPEDFLKLFIDPNEVYCSEASPGSDSGISEDPCHPDPPAPRATSSPMLYEVVYEAG
LZIP 1" MELELDAGDQDLLAFLLEESGDLGTAPDEAVRAPLDWALPLSEVPDWEVDDDL
HP10562 121' ALERMQGETGPNVGLISIQLDQWSPAFMTVPDSCMVSELPFDAHAHILPRAGTVAPVPCTT
LZIP 54" LCSLLSPPASLNILSSSNPCLVHHHTYSLPRETVSMDLESESCRKEGTQMT PQHMEELA
HP10562 181' LLPCQTLFTDEEKRLLGQEGVSLPSHLPLTKAEERVLKVRRKIRNKQSAQDSRRRRKKE
LZIP 114" EQEIARLVLTDEEKSLLKEGLILPETLPLTKTEEQILKRVRRKIRNKRSQAQESRRKKKV
HP10562 241' YIDGLESVAACSAQNQELQKKVQELERHNISILVAQLRQLQTLIAQTSNKAQTSTCVLI
LZIP 174" YVGGLESVLKYTAQNMELQNKVQLLEEQNLSLLDQLRKLQAMVIEISNKTSSSSTCILV
HP10562 301' LLFSLALIILPSFPQSR---PEAGEDYQPHGVTSRN--ILTHKDVTENLETQVWVES
LZIP 234" LLVSFCLLVPMYSSDTRGSLPAEHGVLRSQRLRALPSEDYPQLELPAQSEVPKDSHQ
HP10562 355' RLREPPGAKDANGSTRTLLEKMGKPRPSGRIRSVLHADEM
LZIP 294" WLDGSDCVLQAPGNTSCLLHYMPQAPSAEPPLEWFPFDLFSEPLCRGPILPLQANLTRKG

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Fig. 25

[illegible]

Fig. 26

HP10498 1' MATPSLRGRLARFGNPRKPVLPKNKPLILANRV-GERRREKGEATCITEMSVVMA
 CEC24 1" MMFSSPLLKEKALARGKSIYPKVAVFSEILPLASKNRVQAGQKPRAASSCTQELQALFG
 * * * * * * *
 HP10498 55' CWKQNEFRDDACRKEIQGFLDCAAR-AQEARKMR--SIQETLGESGSLLPNKNLKLQRF
 * * . * * * . * . . . * * * * *
 CEC24 61" CLKKWEFFDDVPCSKQHTLYMDCVHKGAEEAAAYRDATRKGTLGESGAGGKQSMTSAQFNK
 HP10498 112' PNKPYL
 CEC24 121" IQKLFPQPDLGKQPYRQMKRLPTQDYADDTFHRKHWSGKRS

12-03-1961
 08-11-1961

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HP10505 1' MAKHLKFIAFTVMVQEGNVESAYRTLNRILTMGLIEDIKHRRYYEKPCCRRRQRRESYERC  
      ***...*. * * * *  
CEF29 1" MVQNNDVDGAFGLNRLMDSEGMLKIIRRTQFYQKPYMQRKTLMSMEAS  
  
HP10505 61' RRIYNMEMARKINFLMRKNRADPWQGC  
      *. * . * . * . * . * . *  
CEF29 49" TAIFNEDMNRKMFKLVRKNRPDKHPGGQVTIS
```

Fig. 28

HP10515 1' MFLTAL-LWRGRI PGRQWIGKRRRPRFVSLRAKQNMIRRL EIEAENHYWLSMPYMTREQE
* * * * * . * * * * . * * * * * . * * * * . * * * * *
DM63B 1" MHLTLINLFKKTVPGHIFRGKRRRLVKPVSQRAMD TLTREYERQEQVMLLLRRHPYLTMEQS

HP10515 60' RGHA-AVRRREA FEA--IKAAATSKFPPHRFIADQLDHLNVTKKWS
* * * * * . * * * * . * * * * * . * * * * . * * * * *
DM63B 61" FGHAKELOKREKLVARWTDEQTLRKMKPHVTIEERLNQLKIKEAWD



Fig. 29

HP01124	1'	MGTEKESPEPDCQKQFQAASVQNLPKNGSYRPSYEMLRFYSYKQATMGPCLVPRPG
		* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
HSACBP	1'	MSQAEFEKAAEEVRHL----KTKPSDEMLFIYGHYKQATVGDINTERPG
HP01124	60'	FWDPIGRYKWDANSLGKMSREEAMSAYITEMKLVAQKVIDTVPLGEVAEDMFGYFEPLY
		. * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
HSACBP	47"	MLDFTGKAKWDANWELKGTSKEDAMKAYINKVEELKKKYGI

[illegible]

Fig. 31

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HP10101 1' MKA VKSERERGSRRRRHRDGDVVLPA GVVVKQERLSPEVAPPAHRRPDPHSGSPSPPTSEEP
HP10101 60' ARSGHRGNRAGVSRSPPKKNKASGRRSKSPRSKNNRSPHSHSTVKVKQEREDHPRRGRE
CEC32E8 1' MGRDSPDRRRHRDRSPERRRRSRSRDRQTRRD-T
HP10101 121' DRQHREPSEQEHRRA RNSDRDRHRGHS HQRTSNERP GSGQGQGRDRTQNLQAQEEERE
CEC32E8 36" RRDDSPKIKREVKEEQFSDNDSPPRRRRDRGGRDRDRDRNRDDR-RDHRDDRGDRDRDR
HP10101 181' FYNARRREHRQRNDVGGGSESQELVPRPGNNKEKEVPAKEKPSFELSGALLEDNTFR
CEC32E8 95" NF--RRPDPVREDGKQYGLEKKEENWGKPEEPAKEK-----EKVNLGTSGALTEDNTFR
HP10101 241' GVVIKYSEPPEARIPKKRWRLYPFKNDEVLPVMYIHRQSA YLLGRHRRRIADIPIDHPSCS
CEC32E8 148" GVVIKYNPEPPEAKPNARWRLYPFKGEESLQVLYIHRQSA YLLIGRDHKIADIPVDHPSCS
HP10101 301' KQHAVFQYRLVEYTRADGTVGRRRVKPYIIDLGSGNGTFLNNKRIEPQRYYELKEKDLKF
CEC32E8 208" KQHAVLQFRSMPFTRDDGTKARRIMPYIIDLGSGNGTFLNEKKIEPQRYIELQEKDLKF
HP10101 361' GFSSREYVLLHESSTSEIDRKODEDEEEEEFEVSDS
CEC32E8 268" GFSTREYVVMKEREITEEELAEGEDVVKKEESD

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Fig. 32

HP10370 1' MEYDEKLARFRQAHLNPFNKQSGPRQHEQGPGEEVDPVTPEKALPELPPGEPEF
DMCG115 1" MSSWKDGLTSIPGTVAQLINESASNLLHASSTLGSTVGLGGSGTGGSEAGGSEESGPQ
HP10370 55' RCPERVMDLGLSEDHFSRPVGLFLASDVQQLRQAIEECKQVILELPEQSEKQKDAVVRLI
...*...*...*...*...*...*...*...*...*...
DMCG115 61" GAERYRALPIPASLVREQWRRLIFTSANIQDLQAAIAHCRDLVLLSEELSEERRWLVRHLV
HP10370 115' HLRKLQELKDPNE-----DEPNIRVLLHRF-----YKEKSKSVKQTCDK
**...*...*...*...*...*...*...*...*...*...
DMCG115 121" DLRYSLQELEEAQEHSLSGDMVMNAIRAVVGHFVPHPHHGKRNRLQAAAKRNYCDH
HP10370 156' CNTIIWGLIQTWYTCGYRCHSKCLNLISKPCVSKVSHQAEYELNICPEYGLDSQDY
......*...*...*...*...*...*...*...*...*...*...*...*...*...*...
DMCG115 181" CTTIWSVVQNSXVCSDCGFLVHQKIDGVKRVCAHVLVSERHQPISEICPEIGLASQGY
HP10370 216' RCAECHRAPISLRGVSEARQCDYTGQYYCSHCHWNDLAVIPARVVHNWDFEPRKVSRCSM
......*...*...*...*...*...*...*...*...*...*...*...*...*...*...
DMCG115 241" KCAECGTMLNKNFTWIEPRLCDYSGLYCPCRCNWNDSNFIPARIHNWDFSPRRVSR TAL
HP10370 276' RYLALMVHRPVLRLREINPLLFYSYVEELVEIRKLQRDILLMKPYFITCREAMEARLL-LQ
......*...*...*...*...*...*...*...*...*...*...*...*...*...*...
DMCG115 301" QETRLFLNKP LIRLEEDNPKLFVFEKLCVAKKLRLQNLVHMRHYLAACKIASLKLVDQQ
HP10370 335' LQDRQHFEVND EYSVQDLDVHAGRLGCSLTEIHTLFAKHKLDCCERCQAKGFVCELCR
......*...*...*...*...*...*...*...*...*...*...*...*...*...*...
DMCG115 361" LGVRRHLAQSN EYVSLSDLSVESGALSEFLQGVFKAFNDHIR-SCPMCLAQAYICEICS
HP10370 395' EGDVLEFFDSDHTSV CADCBAVFHRDCYTDNSTTCKPKCARLSLRKQSLFQEPGPDVEA
...*...*...*...*...*...*...*...*...*...*...*...*...*...*...*...*...
DMCG115 420" NNEVTFPFDGCIKCDQCN SIFHRVCLTRKNMICPKCIRIQERRLQLDRMKSTEDDDDDDD

Fig. 33

HP10427 1' MAGPAAAFRRRLGALSGAAALGFASYGAH--GAQFPDAYGKELFDKANKHHFLHSLALIG
 ... ***** * .. ** *****.
 CEY106G 1" MSPIIRLAGLSGAVAISLGAYGSHVLRDNPISIDERRRTAFDTASRYHLIHSALLA

 HP10427 58' VPHCRKPLWAGLLLIASGTTLFCFTSFYYQALSGDPSIQTLAPAGGTLLLLGWLALAL
 * * ** * .. ** * * * * *
 CEY106G 57" SPAARFPLVTAGLFTAGITLFCGPCYHYSISGVETTRKYTPIGGVTLIIAWLSFIL

Fig. 34

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HP10516 1' MAGTGLLALRTLPGPSWVRGSPSVLSRLQDAAVVRPGFLSTAEETLSRELEPELRRRR
DMCG141 1"      *...*** * *...** *
MRIITDFISEPEEQQLHEEIEPYMSRLR

HP10516 61' YEYDHWDAAIHGFRETEKSRWSEASRAILQRVQAAAFPGQTLSSVHVLDLEARGYIKP
DMCG141 29" YEFDHWDDAIHGFRETERKKWFPKNREILERVRQVAF--DGAVMPYVHILDLPDGVIKP
      *...*** *...*** *...*** *...*** *...*** *...*** *...*** *...***
      *...*** *...*** *...*** *...*** *...*** *...*** *...*** *...***

HP10516 121' HVDSIKFCGATIAGLSLLSPSVMRLVHT-----QEPG
DMCG141 87" HVDSTRYCGNTISGISLSDSVMRLVVRTDEQRYQQSSGTATDPNSQGSSEPDAAYRHQPE
      *...*** *...*** *...*** *...*** *...*** *...*** *...*** *...***

HP10516 153' EWL-----ELLLEPGSLYILRGSARYDFSHEILRDEESFFGERRIPRGRRISVICRSLP
DMCG141 147" ASLKNNFYADILLPRRSLYIMSHRTARYKFTHEILAKEHSQFQGALVPRTRRRIIICRNEP
      *...*** *...*** *...*** *...*** *...*** *...*** *...*** *...***

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Fig. 35

HP10580	1'		MKKFFQEFKADIKFK
DMCG546	61"		** ...
HP10580	16'		TLRKVLIVLLGTCVLGYSWSIYGKVI TEKFFVRPSTLKEIEELKLSKAEAAFKLNLTG
DMCG546	121"		SAGPGQKLKESVGEKAHKEKPNQ--PAPRPPRQGP TNEAQM AAAAALARLEKQKQSRWGP
HP10580	74'		TSQDTIRNQVRKELQAEATVSGSP-EAPGTNVVSEPREEGSA-HLAVPGVYFTCPL-TGA
DMCG546	180"		TSLSAVKAQA KRELEAERRQREEAMGTPSTSTSTASGGDTRNLACEGVFFRCPLISEE
HP10580	131'		TLRKQORDACIKEAILLHFSTDPVAASIMKIYTFNKDQDRVKLGVDTLAKYLDNIHLHPE
DMCG546	240"		ILPKSVWKVRIKEFLYQQLEADRGLTACLIHNCN-VKEKADECIATLIRYLENLIKNPE
HP10580	191'		EEKYRKIKLQNKVFQERINCLGTHEFFEAIGFQKVL LPAQDQEDPEEFYVLSETTLAQP
DMCG546	299"		EEKFCKIRMSNKFISEKVRVVEGALDVLQAAGFNEV-----QIDGEPFLLTWKEQTEKD

Fig. 35-1

35/1/35

HP10580 251' QSLERHKEQLLAEPVRAKLDQRQRRVFQPSPLASQFELPGDFFNLTAEEIKREQRLRSEA
 * * * * * . * * * * * . * * * * * . * * * * * . * * * * * . * * * * *
 DMC546 353" LDLPTLVEALKSSEIIPLELDNRNIKVLLPSQ-ACRVALPDEFYRLSPEEIKKEQQLRSEA

HP10580 311' VERLSVLRTKAMREKEEQRLRKYNITLLRVRLPDGCLLQGTFYARERLGAVYGFVREAL
 * * * * * . * * * * * . * * * * * . * * * * * . * * * * * . * * * * *
 DMC546 412" IAQSQMLRTKAMREKEEQRLRMRYALVRVKFPNGLFIQGTENVYEKISDVFEFVQSCL

HP10580 371' QSDWLPFELLASGGQKLSEDE-NLALNECGLVPSALLTFSSWDMAVLEDIKAAGAEPSIL
 ... * * * * * . * * * * * . * * * * * . * * * * * . * * * * * . * * * * *
 DMC546 472" ADESLDFSLVNSDGLGDEDEKTLYDCKLI PNTLLLF SANDTPAPLQTDINYLKEDLL

HP10580 430' KPELLSAIEKLL

DMC546 532" MLVQAM